Exhibit A

Clean Version of The Pending Claims in U.S. Patent Application Ser. No. 09/975,308

1. (Amended) An isolated expression vector comprising the nucleotide sequence of SEQ ID NO:8.

2. (Amended) An isolated expression vector comprising a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:9.

3. (New) A host cell comprising the recombinant expression vector of claim 1 or 2.

BD144530 ACCESSION:BD144530 NID: gi 27850288 dbj BD144530.1 Novel
        G-protein coupled receptors
        Length = 924

 Score = 617 bits (1574), Expect = e-174
 Identities = 305/307 (99%), Positives = 307/307 (99%)
 Frame = +1

Query: 1   MNHSVVTEFIILGLTKKPELQGIIFLFFLIVYLVAFLGNMLIIIAKIYSNTLHTPMYVFL 60
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Sbjct: 1   MNHSVVTEFIILGLTKKPELQGIIFLFFLIVYLVAFLGNMLIIIAKIYNNTLHTPMYVFL 180

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Sbjct: 181 LTLAVVDIICTTSIIPKMLGTMLTSENTISYAGCMSQLFLFTWSLGAEMVLFTTMAYDRY 360

Query: 121 VAICFPLHYSTIMNHHMCVALLSMVMAIAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPP 180
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Query: 181 LLALSCSPVRINEVMVYVADITLAIGDFILTCISYGFIIVAILRIRTVEGKRKAFSTCSS 240
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Sbjct: 541 LLALSCSPVRINEVMVYVADITLAIGDFILTCISYGFIIVAILRIRTVEGKRKAFSTCSS 720

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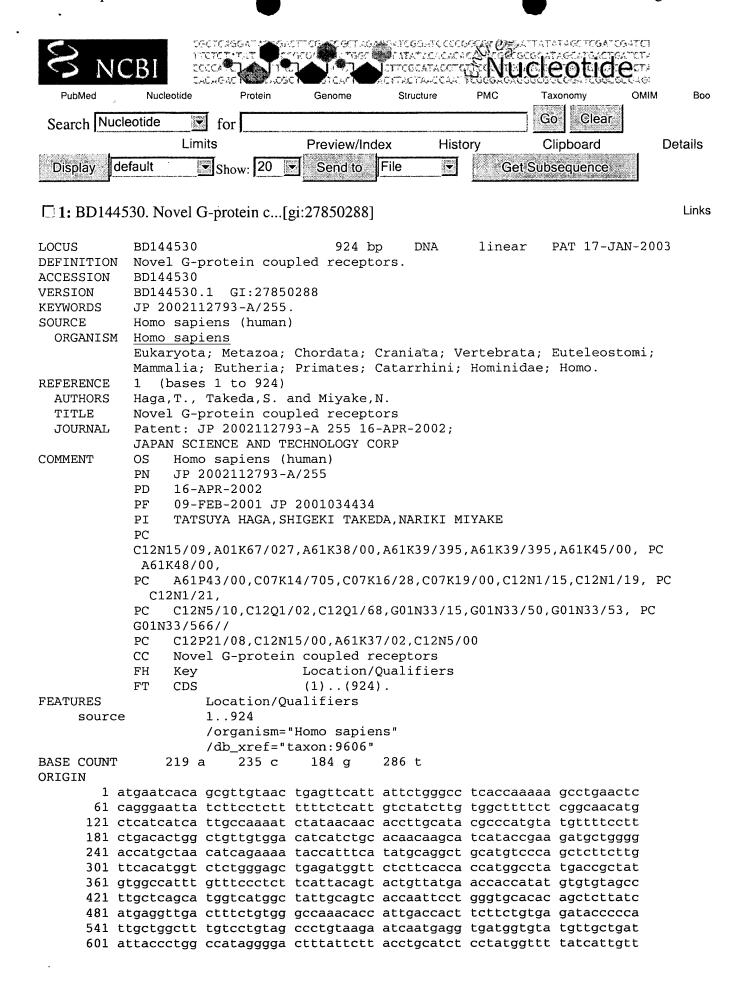   HLTVVTLYYSPVIYTYIRPASSYTFERDKVVAALYTLVTPTLNPMVYSFQNREMQAGIRK
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NCBI

Nucleotide

Search | Nucleotide ▾ | for | _____ | Go   Clear

Limits   Preview/Index   History   Clipboard   Details

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□ **1: BD144530. Novel G-protein c...[gi:27850288]**   Links

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LOCUS       BD144530                924 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel G-protein coupled receptors.
ACCESSION   BD144530
VERSION     BD144530.1  GI:27850288
KEYWORDS    JP 2002112793-A/255.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 924)
  AUTHORS   Haga,T., Takeda,S. and Miyake,N.
  TITLE     Novel G-protein coupled receptors
  JOURNAL   Patent: JP 2002112793-A 255 16-APR-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
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            PD   16-APR-2002
            PF   09-FEB-2001 JP 2001034434
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//

Revised: July 5, 2002.

Feb 19 2003 14:49:48

Query= SEQ ID NO:8
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Sequences producing significant alignments:	(bits)	Value

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 Score = 1824 bits (920), Expect = 0.0
 Identities = 923/924 (99%)
 Strand = Plus / Minus

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NCBI | Nucleotide

PubMed   Nucleotide   Protein   Genome   Structure   PMC   Taxonomy   OMIM   Boo

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☐ **1: AC091612. Homo sapiens chro...[gi:18497169]**   Links

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LOCUS          AC091612               180657 bp    DNA     linear   HTG 05-FEB-2002
DEFINITION     Homo sapiens chromosome 1 clone RP11-656O22, WORKING DRAFT
               SEQUENCE, 1 unordered piece.
ACCESSION      AC091612 AL390860
VERSION        AC091612.4  GI:18497169
KEYWORDS       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE         Homo sapiens (human)
  ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1  (bases 1 to 180657)
  AUTHORS      Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
  TITLE        Direct Submission
  JOURNAL      Unpublished
REFERENCE      2  (bases 1 to 180657)
  AUTHORS      Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J., Ivey,R.G. and
               Haugen,E.D.
  TITLE        Direct Submission
  JOURNAL      Submitted (09-MAY-2001) Genome Center, University of Washington,
               Box 352145, Seattle, WA 98195, USA
COMMENT        On Feb 5, 2002 this sequence version replaced gi:15487406.
               -------------- Genome Center
                   Center: University of Washington Genome Center
                   Center Code: UWGC
                   Web site: http://www.genome.washington.edu
                   Contact: uwgchtgs@u.washington.edu
                   Drafting Center: SC
               -------------- Project Information
                   Center project name: chr-1
                   Center clone name: RP11-656O22 (sc0182)
               ------------- Summary Statistics
                   Sequencing vector: plasmid; L08752; 100% of reads
                   Chemistry: Dye-terminator Big Dye; 100% of reads
                   Assembly program: Phrap; version 0.990319
                   Consensus quality: 180536 bases at least Q40
                   Consensus quality: 180650 bases at least Q30
                   Consensus quality: 180657 bases at least Q20
                   Insert size: 194815; 11.0% error; agarose-fp
                   Insert size: 180657; sum-of-contigs
                   Quality coverage: 8.4x in Q20 bases; agarose-fp
                   Quality coverage: 9.0x in Q20 bases; sum-of-contigs
               --------------.
             * NOTE: This is a 'working draft' sequence. It currently
             * consists of 1 contigs. The true order of the pieces
             * is not known and their order in this sequence record is
             * arbitrary. Gaps between the contigs are represented as
             * runs of N, but the exact sizes of the gaps are unknown.
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